Amendments to the Specification

Please replace paragraph 13 with the following rewritten paragraph:

[13] Table 4, column 1, provides a nucleotide sequence identifier, "SEQ ID NO:X," that matches a nucleotide SEQ ID NO:X disclosed in Table 1, column 5. Table 4, column 2, provides the chromosomal location, "Cytologic Band or Chromosome," of polynucleotides corresponding to SEQ ID NO:X. Chromosomal location was determined by finding exact matches to EST and cDNA sequences contained in the NCBI (National Center for Biotechnology Information) UniGene database. Given a presumptive chromosomal location, disease locus association was determined by comparison with the Morbid Map, derived from Online Mendelian Inheritance in Man (Online Mendelian Inheritance in Man, OMIM™. McKusick-Nathans Institute for Genetic Medicine, Johns Hopkins University (Baltimore, MD) and National Center for Biotechnology Information, National Library of Medicine (Bethesda, MD) 2000. World Wide Web URL[[: http://]]www.ncbi.nlm.nih.gov/omim[[/]]). If the putative chromosomal location of the Query overlapped with the chromosomal location of a Morbid Map entry, the OMIM reference identification number of the morbid map entry is provided in Table 4, column 3, labelled "OMIM ID."

Please replace paragraph 157 with the following rewritten paragraph:

[157] Any polypeptide sequence contained in the polypeptide of SEQ ID NO:Y, encoded by the polynucleotide sequences set forth as SEQ ID NO:X, or encoded by the cDNA in cDNA plasmid:V may be analyzed to determine certain preferred regions of the polypeptide. For example, the amino acid sequence of a polypeptide encoded by a polynucleotide sequence of SEQ ID NO:X or the cDNA in cDNA plasmid:V may be analyzed using the default parameters of the DNASTAR computer algorithm (DNASTAR, Inc., 1228 S. Park St., Madison, WI 53715 USA~~; http://www.dnastar.com/~~).

Please replace paragraph 786 with the following rewritten paragraph:

[786] Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of c - d, where both c and d correspond to the positions of nucleotide residues shown in SEQ ID NO:X, and where d is greater than or equal to c + 14. In no way is this listing meant to encompass all of the sequences which may be excluded by the general formula, it is just a representative example. ~~All references available through these accessions are hereby incorporated by reference in their entirety.~~ The

Public Accession Numbers referenced in Table 2 refer to Accession Numbers in GenBank®, available online at www.ncbi.nlm.nih.gov.